

FILE 'BIOSIS, MEDLINE, CAPLUS' ENTERED AT 14:28:46 ON 05 FEB 2003

L1	8 S CGI (1A) 69
L2	2 S CGI 69
L3	8 S CGI-69
L4	8 S L1 OR L2 OR L3
L5	6 DUP REM L4 (2 DUPLICATES REMOVED)

L Number	Hits	Search Text	DB	Time stamp
1	0	cgi69	USPAT	2003/02/05 14:22
3	36	cgi same "69"	USPAT; US-PGPUB; EPO; DERWENT	2003/02/05 14:22
2	12	cgi same "69"	USPAT	2003/02/05 14:23
4	0	cgi same "69" same metabol\$	USPAT	2003/02/05 14:24
5	0	cgi near4 "69" same metabol\$	USPAT	2003/02/05 14:24
6	0	cgi near6 "69" same metabol\$	USPAT	2003/02/05 14:24

L5 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2003 ACS
 ACCESSION NUMBER: 2001:935655 CAPLUS
 DOCUMENT NUMBER: 136:65246
 TITLE: Protein and cDNA sequences of human and mouse
CGI-69, and methods and uses thereof
 for treating metabolic disorders
 INVENTOR(S): Lewin, David; Adams, Sean H.; Yu, Xing Xian
 PATENT ASSIGNEE(S): Genentech, Inc., USA; Curagen Corporation
 SOURCE: PCT Int. Appl., 107 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001098355	A2	20011227	WO 2001-US20117	20010622
WO 2001098355	A3	20021003		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,				
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,				
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,				
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ,				
VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,				
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,				
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002103150	A1	20020801	US 2001-888264	20010622
US 2002119137	A1	20020829	US 2001-888358	20010622
PRIORITY APPLN. INFO.:			US 2000-213307P	P 20000622

AB The invention provides protein and cDNA sequences of human and mouse
CGI-69 and of a novel human splice variant (**CGI-69L**).
 The invention relates to the characterization of **CGI-69**
 as a putative mitochondrial carrier protein, and to the discovery of the
 alteration of the mitochondrial membrane potential through the
 overexpression of carboxy-FLAG-tagged **CGI-69**. The
 invention also relates to the use of the **CGI-69**
 protein and/or **CGI-69**-encoding nucleic acids in
 diagnosing or treating metabolic diseases, such as obesity and cachexia.
 The invention also relates to the use of the **CGI-69**
 protein/nucleic acids in drug screening assays.

L5 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
 ACCESSION NUMBER: 2001:81198 BIOSIS
 DOCUMENT NUMBER: PREV200100081198
 TITLE: Overexpression of the human 2-oxoglutarate carrier lowers
 mitochondrial membrane potential in HEK-293 cells: Contrast
 with the unique cold-induced mitochondrial carrier
CGI-69.
 AUTHOR(S): Yu, Xing Xian; Lewin, David A.; Zhong, Alan; Brush,
 Jennifer; Schow, Peter W.; Sherwood, Steven W.; Pan,
 Guohua; Adams, Sean H. (1)
 CORPORATE SOURCE: (1) Department of Endocrinology, Genentech, Inc., 1 DNA
 Way, South San Francisco, CA, 94080: shadams@gene.com USA
 SOURCE: Biochemical Journal, (15 January, 2001) Vol. 353, No. 2,
 pp. 369-375. print.
 ISSN: 0264-6021.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English
 AB Using differential mRNA expression analysis, a previously uncharacterized
 gene was found to be up-regulated 2-fold in brown adipose tissue (BAT) of

mice exposed to cold (4 degreeC) for 48 h. Contig and homology analysis revealed that the gene represents the murine orthologue to a sequence from a public database encoding a putative human protein (**CGI-69**). The presence of mitochondrial carrier domains in the human protein, its transmembrane topology and cold-induction of the mouse **CGI-69** gene in BAT prompted an analysis of the idea that **CGI-69** may represent a new uncoupling protein (UCP) functional homologue. However, transfection of human **CGI-69** isoforms in HEK-293 cells yielded no change in mitochondrial membrane potential (DELTApsim), despite localization of FLAG-tagged **CGI-69** to mitochondria of MCF7 cells. Surprisingly, overexpression of the human 2-oxoglutarate carrier (OGC) protein (originally designed as a negative control) sparked a significant drop in DELTApsim, possibly signalling a previously unappreciated uncoupling activity for the OGC.

L5 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:198833 BIOSIS
 DOCUMENT NUMBER: PREV200200198833
 TITLE: Defining the distal structural and functional organization of the megakaryocyte-specific alphaIIb gene.
 AUTHOR(S): Thornton, Michael A. (1); Cheng, Jan-Fang; Zhang, Chunyan (1); Rubin, Edward M.; Poncz, Mortimer (1)
 CORPORATE SOURCE: (1) Department of Pediatrics, Children's Hospital and University of Pennsylvania, Philadelphia, PA USA
 SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 283a. <http://www.bloodjournal.org/>. print.
 Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11, 2001
 ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English

AB The alphaIIb gene has been studied as a model for megakaryocyte-specific expression. These studies have focused on the immediate 5'-flanking region. Taking advantage of the human and mouse genome projects, we have completed an analysis of the alphaIIb gene locus using the AVID/mVISTA global alignment program, which was developed for the purpose of annotation and biological discovery using large (>100 kb) orthologous genomic sequences from two species. The source material for this study was derived from our own sequences and from the GenBank public database, for the human and murine alphaIIb gene loci. This study compared a region extending from 62 kb upstream of the alphaIIb gene start site to 120 kb downstream of its last exon. The results of these comparative studies indicate that the nucleotide sequences for the coding regions of many genes including the KIAA-0553; Granulin, **CGI-69**, RPIP8 and the SLC4A1/EPB3 genes which surround the alphaIIb gene as well as the alphaIIb gene itself, are highly conserved ranging from 75% to 95% homology. Moreover, a number of non-coding regions intergenic between the alphaIIb gene and its nearest 5' and 3' neighbors, KIAA-0553 and Granulin, respectively, also exhibited conservation. Two of these non-coding regions located -3.8 to -4.2 kb upstream of the alphaIIb start site and a second region 4.3 to 6.1 kb downstream of the last alphaIIb exon were conserved 72% and 85%, respectively, and contain several conserved GATA-binding sites which could potentially bind GATA-1, a transcription factor important in megakaryopoiesis. To examine the potential functional significance of the two highly conserved flanking regions, we analyzed them using both DNase I hypersensitive (HS) studies and transgenic animal analysis. We found that both the 5'- and 3'-conserved flanking domains were coincident with DNase I HS sites. Further, at least the 5' DNase I HS was tissue-specific, thus indicating a preferential open chromatin state within alphaIIb expressing cell lines. Transgenic mice lines that carried the entire human alphaIIb coding region (exons and introns) and either the

5'- or 3'-conserved regions or both were analyzed. Transgenic lines possessing only the intact gene could direct tissue-specific expression, but only at a level 103-104-fold lower than the native mouse message. Inclusion of the conserved 5' domain did not affect the level of expression, but lead to copy-number dependent expression. However transgenic lines which included both the 5' and 3' conserved domains expressed at levels that were comparable to or higher than native levels, suggesting that the 3' domain contains a critical enhancer element. Thus, our studies have defined the distal organization of the alphaIIb gene and demonstrate conserved domains within the flanking regions. These conserved domains coincide with sites of open chromatin structure and coincide with critical functional elements involved in consistent and high level of expression. Analysis of the mechanisms by which these conserved domains contribute to alphaIIb gene expression should provide important insights into the mechanisms by which specific genes are expressed during megakaryopoiesis.

L5 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2000:353373 CAPLUS

DOCUMENT NUMBER: 133:277011

TITLE: Identification of novel human genes evolutionarily conserved in *Caenorhabditis elegans* by comparative proteomics

AUTHOR(S): Lai, Chun-Hung; Chou, Chang-Yuan; Ch'ang, Lan-Yang; Liu, Chung-Shyan; Lin, Wen-Chang

CORPORATE SOURCE: Institute of Biomedical Sciences, Academia Sinica, Taipei, 115, Taiwan

SOURCE: Genome Research (2000), 10(5), 703-713

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Modern biomedical research greatly benefits from large-scale genome-sequencing projects ranging from studies of viruses, bacteria, and yeast to multicellular organisms, like *Caenorhabditis elegans*. Comparative genomic studies offer a vast array of prospects for identification and functional annotation of human ortholog genes. We presented a novel comparative proteomic approach for assembling human gene contigs and assisting gene discovery. The *C. elegans* proteome was used as an alignment template to assist in novel human gene identification from human EST nucleotide databases. Among the available 18,452 *C. elegans* protein sequences, our results indicate that at least 83% (15,344 sequences) of *C. elegans* proteome has human homologous genes, with 7954 records of *C. elegans* proteins matching known human gene transcripts. Only 11% or less of *C. elegans* proteome contains nematode-specific genes. We found that the remaining 7390 sequences might lead to discoveries of novel human genes, and over 150 putative full-length human gene transcripts were assembled upon further database analyses.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:64506 CAPLUS

DOCUMENT NUMBER: 137:91258

TITLE: ES cell neural differentiation reveals a substantial number of novel ESTs. [Erratum to document cited in CA135:150370]

AUTHOR(S): Bain, G.; Mansergh, F. C.; Wride, M. A.; Hance, J. E.; Isogawa, A.; Rancourt, S. L.; Ray, W. J.; Yoshimura, Y.; Tsuzuki, T.; Gottlieb, D. I.; Rancourt, D. E.

CORPORATE SOURCE: Department of Oncology Department of Biochemistry and Molecular Biology, The University of Calgary, Calgary, AB, T2N 4N1, Can.

SOURCE: Functional & Integrative Genomics (2000), 1(3),
218-219
CODEN: FIGUBY; ISSN: 1438-793X
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The captions for Fig. 1 and Fig. 2 were reversed.

L5 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:59749 CAPLUS
DOCUMENT NUMBER: 135:150370
TITLE: ES cell neural differentiation reveals a substantial
number of novel ESTs
AUTHOR(S): Bain, G.; Mansergh, F. C.; Wride, M. A.; Hance, J. E.;
Isogawa, A.; Rancourt, S. L.; Ray, W. J.; Yoshimura,
Y.; Tsuzuki, T.; Gottlieb, D. I.; Rancourt, D. E.
CORPORATE SOURCE: Department of Oncology, Department of Biochemistry and
Molecular Biology, The University of Calgary, Calgary,
AB, T2N 4N1, Can.
SOURCE: Functional & Integrative Genomics (2000), 1(2),
127-139
CODEN: FIGUBY; ISSN: 1438-793X
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A method was used for synchronously differentiating murine embryonic stem
(ES) cells into functional neurons and glia in culture. Using subtractive
hybridization, .apprx.1200 cDNA clones were isolated from ES cell cultures
at the neural precursor stage of neural differentiation. Pilot studies
indicated that this library is a good source of novel neuro-embryonic cDNA
clones. Therefore, the entire library was screened by single-pass
sequencing. Characterization of 604 non-redundant cDNA clones by BLAST
revealed 96 novel expressed sequence tags (ESTs) and an addnl. 197
matching uncharacterized ESTs or genomic clones derived from genome
sequencing projects. With the exception of a handful of genes, whose
functions are still unclear, most of the 311 known genes identified in
this screen are expressed in embryonic development and/or the nervous
system. At least 80 of these genes are implicated in disorders of
differentiation, neural development, and/or neural function. This study
provides an initial snapshot of gene expression during early neural
differentiation of ES cell cultures. Given the recent identification of
human ES cells, further characterization of these novel and
uncharacterized ESTs has the potential to identify genes that may be
important in nervous system development, physiolo., and disease.

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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